

SEQUENCE LISTING

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RASMUSSEN, Grethe
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SCHAMBYE, Hans Thalsgård
ANDERSEN, Kim Vilbour
BORNES, Claus
Maxygen ApS
Maxygen Holdings Ltd.

<120> NEW INTERFERON BETA-LIKE MOLECULES

<130> 0228us410

<150> US 60/272,116

<151> 2001-02-27

<150> US 60/343,436

<151> 2001-12-21

<150> US 60/302,140

<151> 2001-06-29

<150> US 60/316,170

<151> 2001-08-30

<150> not yet assigned

<151> 2002-02-19

<150> DK PA 2001 00333

<151> 2001-03-01

<150> US 09/648,569

<151> 2000-08-25

<160> 57

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<213> Homo sapiens

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<221> CDS

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Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu

1

5

10

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ttg tgc ttc tcc act aca gct ctt tcc atg agc tac aac ttg ctt gga 159
Leu Cys Phe Ser Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly
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ttc cta caa aga agc agc aat ttt cag tgt cag aag ctc ctg tgg caa 207
Phe Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln
      30                35                40

ttg aat ggg agg ctt gaa tac tgc ctc aag gac agg atg aac ttt gac 255
Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp
      45                50                55                60

atc cct gag gag att aag cag ctg cag cag ttc cag aag gag gac gcc 303
Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala
      65                70                75

gca ttg acc atc tat gag atg ctc cag aac atc ttt gct att ttc aga 351
Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg
      80                85                90

caa gat tca tct agc act ggc tgg aat gag act att gtt gag aac ctc 399
Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu
      95                100                105

ctg gct aat gtc tat cat cag ata aac cat ctg aag aca gtc ctg gaa 447
Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu
      110                115                120

gaa aaa ctg gag aaa gaa gat ttc acc agg gga aaa ctc atg agc agt 495
Glu Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser
      125                130                135                140

ctg cac ctg aaa aga tat tat ggg agg att ctg cat tac ctg aag gcc 543
Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala
      145                150                155

aag gag tac agt cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta 591
Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu
      160                165                170

agg aac ttt tac ttc att aac aga ctt aca ggt tac ctc cga aac 636
Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
      175                180                185

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gcagatgctg ttttaagtgc tgatggctaa tgtactgcat atgaaaggac actagaagat 756
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aaattat tttt tggtgcaaaa gtca 840

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 <213> Homo sapiens
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			20					25					30		
Lys	Asp	Arg	Met	Asn	Phe	Asp	Ile	Pro	Glu	Glu	Ile	Lys	Gln	Leu	Gln
			35				40					45			
Gln	Phe	Gln	Lys	Glu	Asp	Ala	Ala	Leu	Thr	Ile	Tyr	Glu	Met	Leu	Gln
			50			55					60				
Asn	Ile	Phe	Ala	Ile	Phe	Arg	Gln	Asp	Ser	Ser	Ser	Thr	Gly	Trp	Asn
65					70				75					80	
Glu	Thr	Ile	Val	Glu	Asn	Leu	Leu	Ala	Asn	Val	Tyr	His	Gln	Ile	Asn
			85					90					95		
His	Leu	Lys	Thr	Val	Leu	Glu	Glu	Lys	Leu	Glu	Lys	Glu	Asp	Phe	Thr
			100					105					110		
Arg	Gly	Lys	Leu	Met	Ser	Ser	Leu	His	Leu	Lys	Arg	Tyr	Tyr	Gly	Arg
			115				120					125			
Ile	Leu	His	Tyr	Leu	Lys	Ala	Lys	Glu	Tyr	Ser	His	Cys	Ala	Trp	Thr
			130			135					140				
Ile	Val	Arg	Val	Glu	Ile	Leu	Arg	Asn	Phe	Tyr	Phe	Ile	Asn	Arg	Leu
145					150				155						160
Thr	Gly	Tyr	Leu	Arg	Asn										
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<210> 7
 <211> 70
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 agcgctacta 70

<210> 8
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 catcaaccgc 70

<210> 9
 <211> 70
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<210> 10

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ggccagcagg 70

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<210> 13
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1 5

<210> 50
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20 25 30
Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln
35 40 45
Asn Phe Thr Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
50 55 60
Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
65 70 75 80
Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
85 90 95
His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Phe Asn Thr
100 105 110
Thr Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
115 120 125
Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
130 135 140
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145 150 155 160
Thr Gly Tyr Leu Arg Asn
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 Arg Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Arg Gln Leu Gln
 35 40 45
 Asn Phe Thr Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
 50 55 60
 Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
 65 70 75 80
 Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
 85 90 95
 His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Phe Asn Thr
 100 105 110
 Thr Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
 115 120 125
 Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
 130 135 140
 Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu
 145 150 155 160
 Thr Gly Tyr Leu Arg Asn
 165